

SEQUENCE LISTING

<110> Patience, Clive

<120> Gamma Herpes Virus DNA and Methods of Use

<130> 61750-379

<150> US/09/612,204

<151> 2000-07-07

<150> US/60/142,736

<151> 1999-07-08

<150> US/60/168,532

<151> 1999-12-02

<160> 55

<170> PatentIn version 3.0

<210> 1

<211> 585

<212> DNA

<213> artificial

<220>

<223> Fragment from Swine Gamma Herpesvirus DNA coding for glycoprotein B envelope protein

<400> 1

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agcatgattt acaatagacc cgtatcagcc aaaagaatag gagatgtcat ttcagtctct      180
aactgtattg tggtagacca aaccagtgtc tcattacata aaagtctcag gcttctcagt      240
gcatcggatg aaaagtgctt ctctagacct ccagtgcacat ttaagtattat gaatgacagt      300
actattttaca aagggaactt aggagtcaat aatgagattc tcttaaccac aacatacctt      360
gaaacatgtc aggaaaacac tgagtattac tttcaggcaa agacagacat gtacattttac      420
aaaaactatg agcatttgaa gactgtgcct ttatcttcga tcaccacact agatacatTT      480
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<212> PRT

<213> artificial

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<223> Deduced amino acid sequence derived from the first open reading frame of the DNA of SEQ ID NO:

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20050414

20 25 30
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 35 40 45
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 Val Asp Gln Thr Ser Val Ser Leu His Lys Ser Leu Arg Leu Leu Ser
 65 70 75 80
 Ala Ser Asp Glu Lys Cys Phe Ser Arg Pro Pro Val Thr Phe Lys Phe
 85 90 95
 Met Asn Asp Ser Thr Ile Tyr Lys Gly Gln Leu Gly Val Asn Asn Glu
 100 105 110
 Ile Leu Leu Thr Thr Thr Tyr Leu Glu Thr Cys Gln Glu Asn Thr Glu
 115 120 125
 Tyr Tyr Phe Gln Ala Lys Thr Asp Met Tyr Ile Tyr Lys Asn Tyr Glu
 130 135 140
 His Leu Lys Thr Val Pro Leu Ser Ser Ile Thr Thr Leu Asp Thr Phe
 145 150 155 160
 Ile Ala Leu Asn Phe Thr Leu Leu Glu Asn Val Asp Phe Lys Val Ile
 165 170 175
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 180 185 190
 Glu Thr Met
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<210> 3
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<220>
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<400> 3
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19

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<400> 4
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<400> 5
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<210> 13
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<220>
<223> PCR amplification primer for pGHV-gpB gene sequences

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<220>
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<223> PCR amplification primer for Epstein-Barr Virus genome

<400> 15
agaactaccg tcaactgcct                                    20

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<212> DNA
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<220>
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<400> 16
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<210> 17
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<220>
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<400> 17
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<210> 18
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<220>
<223> PCR amplification primer for Epstein-Barr Virus genome

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<210> 21
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<220>
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<400> 21
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<210> 22
<211> 21
<212> DNA
<213> artificial

<220>
<223> PCR amplification primer for Epstein-Barr Virus genome

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<400> 22
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<220>
<223> cDNA for porcine gamma herpesvirus gpB gene

<400> 23
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tgggtctactg aatcgccgct aacagggtcac tatggaacac acgattcaag ccatgggtgaa 180
agaggaaaaca acgaaaacag agattcagaa gagcaaaata aaaacattta tggatcgccct 240
tctacgttttc cttacagagt atgcagtgcc tccggagttg gagatgtctt tagatttcag 300
accgaccatg tgtgtcccga tgccagtgat atggtacaca gtgaggggat tctactaatt 360
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2598 "400" 23

<210> 24
 <211> 865
 <212> PRT
 <213> artificial

<220>

<223> Deduced amino acid sequence of porcine gamma herpesvirus gpB gene

<400> 24

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Leu Tyr Gln Val Ala Leu Tyr Ser Leu Ser Ile Ala Glu Thr Gly Val
 20 25 30

Thr Ser Pro Pro Asn Thr Ala Thr Trp Ser Thr Glu Ser Pro Leu Thr
 35 40 45

Gly His Tyr Gly Thr His Asp Ser Ser His Gly Glu Arg Gly Asn Asn
 50 55 60

Glu Asn Arg Asp Ser Glu Glu Gln Asn Lys Asn Ile Tyr Gly Ser Pro
 65 70 75 80

Ser Thr Phe Pro Tyr Arg Val Cys Ser Ala Ser Gly Val Gly Asp Val
 85 90 95

Phe Arg Phe Gln Thr Asp His Val Cys Pro Asp Ala Ser Asp Met Val
 100 105 110

His Ser Glu Gly Ile Leu Leu Ile Tyr Lys Gln Asn Ile Ile Pro Phe
 115 120 125

Met Phe Arg Val Arg Lys Tyr Arg Lys Val Val Thr Thr Ser Thr Val
 130 135 140

Tyr Asn Gly Ile Tyr Ser Asp Ser Ile Thr Asn Gln His Thr Phe Tyr
 145 150 155 160

Lys Ser Ile Glu Pro Trp Glu Thr Glu Lys Met Asp Thr Ile Tyr Gln
 165 170 175

Cys Phe Asn Ser Leu Arg Leu Asn Thr Gly Gly Asn Leu Leu Thr Tyr
 180 185 190

Val Asp Arg Asp Asp Ile Asn Met Thr Val Phe Leu Gln Pro Val Asp
 195 200 205

Gly Val Thr Pro Asp Val Lys Arg Tyr Gly Ser Gln Pro Glu Leu Tyr
 210 215 220

Leu Glu Pro Gly Trp Phe Trp Gly Ser Tyr Arg Arg Arg Thr Thr Val
 225 230 235 240

Asn Cys Glu Leu Met Asp Met Phe Ala Arg Ser Asn Pro Pro Phe Asp
 245 250 255

Phe Phe Val Thr Ala Thr Gly Asp Thr Val Glu Met Ser Pro Phe Trp
 260 265 270
 Ser Gly Glu Asp Asp His Glu Asn Lys Met His Glu Lys Pro Trp Phe
 275 280 285
 Val Ser Val Ile Asn Asn Tyr Lys Val Val Asp Tyr Gln Asn Arg Gly
 290 295 300
 Thr Val Pro Leu Gly Lys Thr Arg Ile Phe Leu Asp Arg Glu Glu Tyr
 305 310 315 320
 Thr Leu Ser Trp Glu Lys His Leu Lys Asn Met Ser Tyr Cys Pro Leu
 325 330 335
 Thr Leu Trp Lys Ala Phe Tyr Asn Gly Ile Gln Thr Glu His Ser Gly
 340 345 350
 Ser Tyr His Phe Val Ala Asn Asp Ile Thr Ala Ser Phe Thr Thr Ser
 355 360 365
 Lys Glu Asp Met Lys Glu Phe Asn Thr Thr Tyr His Cys Leu Asn Glu
 370 375 380
 Glu Ile Lys Ala Glu Ile Glu Lys Lys Tyr Ala Lys Val Asn Ser Thr
 385 390 395 400
 His Ser Lys Tyr Gly Asp Leu Lys Tyr Phe Lys Thr Asp Gly Gly Leu
 405 410 415
 Tyr Leu Val Trp Gln Pro Leu Ile Gln Asn Arg Leu Leu Asp Ala Lys
 420 425 430
 Asn Lys Leu Asn Asn Glu Thr Tyr Ser Arg Arg Ser Arg Arg Gln Ala
 435 440 445
 Glu Ser Thr Thr Asp Pro Met Met Glu Met Thr Gly Asn Gly Ala Gly
 450 455 460
 Gly Glu Tyr Ser Ser Glu Asn Ser Ile Thr Val Ala Gln Val Gln Tyr
 465 470 475 480
 Ala Tyr Asp Asn Leu Arg Ile Arg Ile Asn Asn Ile Leu Glu Asp Leu
 485 490 495
 Ser Lys Ala Trp Cys Arg Glu Gln His Arg Ala Ala Leu Val Trp Asn
 500 505 510
 Glu Leu Ser Lys Ile Asn Pro Thr Ser Val Met Ser Met Ile Tyr Asn
 515 520 525
 Arg Pro Val Ser Ala Lys Arg Ile Gly Asp Val Ile Ser Val Ser Asn
 530 535 540
 Cys Ile Val Val Asp Gln Thr Ser Val Ser Leu His Lys Ser Leu Arg
 545 550 555 560

Leu	Leu	Ser	Ala	Ser	Asp	Glu	Lys	Cys	Phe	Ser	Arg	Pro	Pro	Val	Thr		
				565					570					575			
Phe	Lys	Phe	Met	Asn	Asp	Ser	Thr	Ile	Tyr	Lys	Gly	Gln	Leu	Gly	Val		
			580					585					590				
Asn	Asn	Glu	Ile	Leu	Leu	Thr	Thr	Thr	Tyr	Leu	Glu	Thr	Cys	Gln	Glu		
		595					600					605					
Asn	Thr	Glu	Tyr	Tyr	Phe	Gln	Ala	Lys	Thr	Asp	Met	Tyr	Ile	Tyr	Lys		
	610					615				620							
Asn	Tyr	Glu	His	Leu	Lys	Thr	Val	Pro	Leu	Ser	Ser	Ile	Thr	Thr	Leu		
	625				630					635					640		
Asp	Thr	Phe	Ile	Ala	Leu	Asn	Phe	Thr	Leu	Leu	Glu	Asn	Val	Asp	Phe		
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Lys	Val	Ile	Glu	Leu	Tyr	Thr	Arg	Asp	Glu	Lys	Arg	Leu	Ser	Asn	Val		
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Phe	Asp	Ile	Glu	Thr	Met	Phe	Arg	Glu	Tyr	Asn	Tyr	Tyr	Ala	Gln	Arg		
		675					680					685					
Val	Ser	Gly	Leu	Arg	Lys	Asp	Leu	Leu	Asp	Leu	Ser	Thr	Asn	Arg	Asn		
	690					695					700						
Gln	Phe	Val	Asp	Ala	Phe	Gly	Ser	Leu	Met	Asp	Asp	Leu	Gly	Ala	Val		
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Gly	Gln	Thr	Val	Val	Asn	Ala	Val	Ser	Gly	Val	Ala	Thr	Leu	Phe	Ser		
				725					730					735			
Ser	Ile	Val	Thr	Gly	Phe	Ile	Asn	Phe	Ile	Lys	Asn	Pro	Phe	Gly	Gly		
		740						745					750				
Met	Leu	Met	Ile	Ile	Val	Val	Ile	Gly	Val	Leu	Phe	Ala	Ile	Tyr	Phe		
		755					760					765					
Leu	Thr	Lys	Lys	Thr	Lys	Ile	Tyr	Glu	Thr	Ala	Pro	Ile	Lys	Met	Ile		
	770					775					780						
Tyr	Pro	Glu	Ile	Asp	Lys	Leu	Lys	Glu	Arg	Glu	Gly	Lys	Ser	Glu	Ile		
	785				790					795					800		
Ala	Pro	Ile	Ser	Glu	Glu	Glu	Leu	Glu	Arg	Ile	Val	Leu	Ala	Met	His		
				805					810					815			
Ile	His	Gln	Gln	Asn	Ser	His	Met	Glu	Thr	Lys	Thr	Arg	Lys	Asp	Pro		
		820						825					830				
Lys	Asp	Ser	Ile	Leu	Thr	Arg	Ala	Gln	Asn	Met	Leu	Arg	Lys	Arg	Ser		
	835						840					845					
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Leu
865

<210> 25
<211> 24
<212> DNA
<213> artificial

<220>

<223> Sequencing primer for TOPO-pCRII: bases 434-458

<400> 25

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24

<210> 26
<211> 17
<212> DNA
<213> artificial

<220>

<223> M13 reverse sequencing primer for TOPO-pCRII: bases 205-222

<400> 26

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17

<210> 27
<211> 20
<212> DNA
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<220>

<223> Sequencing primer for porcine gamma herpesvirus gpB gene: bases
1989-2008

<400> 27

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20

<210> 28
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<220>

<223> Sequencing primer for porcine gamma herpesvirus gpB gene: bases
1513-1531

<400> 28

acaccagagc agctctatg

19

<210> 29
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<220>
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 2399-2422

<400> 29
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<210> 30
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 322-343

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<210> 31
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<220>
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<400> 31
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<210> 32
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<220>
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 537-560

<400> 32
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<210> 33
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<220>
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 815-835

<400> 33

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<210> 34
<211> 25
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<220>
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993-1017

<400> 34
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<210> 35
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<220>
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1073-1093

<400> 35
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<210> 36
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<220>
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1673-1694

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<210> 37
<211> 823
<212> PRT
<213> Human herpesvirus 8

<400> 37
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20 25 30

Thr Ser Ser Ser Pro Thr Pro Pro Gly Ser Ser Ser Lys Ala Pro Thr
35 40 45

Val	Ala	Asn	Phe	Thr	Asp	Thr	Tyr	Ser	Cys	Leu	Thr	Ser	Asp	Ile	Asn	
		355					360					365				
Thr	Thr	Leu	Asn	Ala	Ser	Lys	Ala	Lys	Leu	Ala	Ser	Thr	His	Val	Pro	
		370				375					380					
Asn	Gly	Thr	Val	Gln	Tyr	Phe	His	Thr	Thr	Gly	Gly	Leu	Tyr	Leu	Val	
385					390					395					400	
Trp	Gln	Pro	Met	Ser	Ala	Ile	Asn	Leu	Thr	His	Ala	Gln	Gly	Asp	Ser	
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Gly	Asn	Pro	Thr	Ser	Ser	Pro	Pro	Pro	Ser	Ala	Ser	Pro	Met	Thr	Thr	
			420					425					430			
Ser	Ala	Ser	Arg	Arg	Lys	Arg	Arg	Ser	Ala	Ser	Thr	Ala	Ala	Ala	Gly	
		435					440					445				
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	450					455					460					
Tyr	Asp	Lys	Leu	Arg	Asp	Gly	Ile	Asn	Gln	Val	Leu	Glu	Glu	Leu	Ser	
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Leu	Ser	Lys	Ile	Asn	Pro	Thr	Ser	Val	Met	Thr	Ala	Ile	Tyr	Gly	Arg	
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			580					585					590			
His	Tyr	Phe	Ile	Thr	Arg	Asn	Glu	Thr	Leu	Val	Tyr	Lys	Asp	Tyr	Ala	
		595				600						605				
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Ile	Ala	Leu	Asn	Leu	Ser	Phe	Ile	Gln	Asn	Ile	Asp	Phe	Lys	Ala	Ile	
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			100					105						110		
Lys	Val	Ala	Thr	Ser	Val	Thr	Val	Tyr	Arg	Gly	Trp	Thr	Glu	Thr	Ala	
		115					120					125				
Val	Thr	Gly	Lys	Gln	Glu	Val	Ile	Arg	Pro	Val	Pro	Gln	Tyr	Glu	Ile	
	130					135					140					
Asn	His	Met	Asp	Thr	Thr	Tyr	Gln	Cys	Phe	Ser	Ser	Met	Arg	Val	Asn	
145					150					155					160	
Val	Asn	Gly	Ile	Val	Asn	Thr	Tyr	Thr	Asp	Arg	Asp	Phe	Thr	Asn	Gln	
			165						170					175		
Thr	Val	Phe	Leu	Gln	Pro	Val	Glu	Gly	Leu	Thr	Asp	Asn	Ile	Gln	Arg	
		180						185					190			
Tyr	Phe	Ser	Gln	Pro	Val	Leu	Tyr	Thr	Thr	Pro	Gly	Trp	Phe	Pro	Gly	
		195					200					205				
Ile	Tyr	Arg	Val	Arg	Thr	Thr	Val	Asn	Cys	Glu	Ile	Val	Asp	Met	Ile	
	210					215					220					
Ala	Arg	Ser	Ala	Glu	Pro	Tyr	Ser	Tyr	Phe	Val	Thr	Ala	Leu	Gly	Asp	
225					230					235					240	
Thr	Val	Glu	Val	Ser	Pro	Phe	Cys	His	Asn	Asp	Ser	Thr	Cys	Ser	Val	
			245						250					255		
Ala	Glu	Lys	Thr	Glu	Asn	Gly	Leu	Gly	Ala	Arg	Val	Leu	Thr	Asn	Tyr	
		260						265					270			
Thr	Met	Val	Asp	Phe	Ala	Thr	Arg	Ala	Pro	Thr	Thr	Glu	Thr	Arg	Val	
	275						280					285				
Phe	Ala	Asp	Ser	Gly	Glu	Tyr	Thr	Val	Ser	Trp	Lys	Ala	Glu	Asp	Pro	
	290					295					300					
Lys	Ser	Ala	Val	Cys	Ala	Leu	Thr	Leu	Trp	Lys	Thr	Phe	Pro	Arg	Ala	
305					310					315					320	
Ile	Gln	Thr	Thr	His	Glu	Ala	Ser	Tyr	His	Phe	Val	Ala	Asn	Asp	Val	
			325						330					335		
Thr	Ala	Thr	Phe	Thr	Ser	Pro	Leu	Ser	Glu	Val	Ala	Asn	Phe	Thr	Gly	
		340						345					350			
Thr	Tyr	Ser	Cys	Leu	Asp	Glu	Val	Ile	Gln	Lys	Thr	Leu	Asn	Asp	Thr	
		355					360					365				
Ile	Lys	Lys	Leu	Ser	Asp	Thr	His	Val	Thr	Asn	Gly	Ser	Ala	Gln	Tyr	
	370					375					380					
Tyr	Lys	Thr	Glu	Gly	Gly	Leu	Phe	Leu	Leu	Trp	Gln	Pro	Leu	Thr	Pro	
385					390					395					400	

Leu	Ser	Leu	Val	Asp	Glu	Met	Arg	Gly	Leu	Asn	Gly	Thr	Thr	Pro	Ala	
				405					410					415		
Pro	Pro	Ala	Thr	Thr	Ser	Thr	Val	Ser	Arg	Val	Arg	Arg	Ser	Val	Asn	
			420					425					430			
Thr	Asn	Glu	Gln	Ala	Thr	Asp	Asn	Leu	Ala	Ala	Pro	Gln	Leu	Gln	Phe	
		435					440					445				
Ala	Tyr	Asp	Lys	Leu	Arg	Ala	Ser	Ile	Asn	Lys	Val	Leu	Glu	Glu	Leu	
	450					455					460					
Ser	Arg	Ala	Trp	Cys	Arg	Glu	Gln	Val	Arg	Asp	Thr	Tyr	Met	Trp	Tyr	
465					470					475					480	
Glu	Leu	Ser	Lys	Ile	Asn	Pro	Thr	Ser	Val	Met	Thr	Ala	Ile	Tyr	Gly	
			485						490					495		
Arg	Pro	Val	Ser	Ala	Lys	Phe	Val	Gly	Asp	Ala	Ile	Ser	Val	Thr	Asp	
			500					505					510			
Cys	Val	Ala	Val	Asp	Gln	Ala	Ser	Val	Ser	Ile	His	Lys	Ser	Leu	Arg	
		515					520					525				
Thr	Ser	Thr	Pro	Gly	Met	Cys	Tyr	Ser	Arg	Pro	Pro	Val	Thr	Phe	Arg	
	530					535					540					
Phe	Leu	Asn	Ser	Thr	Thr	Leu	Phe	Lys	Gly	Gln	Leu	Gly	Pro	Arg	Asn	
545					550					555					560	
Glu	Ile	Ile	Leu	Thr	Asp	Asn	Gln	Val	Glu	Ala	Cys	Lys	Glu	Thr	Cys	
			565						570					575		
Glu	His	Tyr	Phe	Ile	Ala	Ser	Asn	Val	Thr	Tyr	Tyr	Tyr	Lys	Asp	Tyr	
		580					585						590			
Val	Phe	Val	Lys	Lys	Ile	Asn	Thr	Ser	Glu	Ile	Ser	Thr	Leu	Gly	Thr	
		595					600					605				
Phe	Ile	Ala	Leu	Asn	Leu	Ser	Phe	Ile	Glu	Asn	Ile	Asp	Phe	Arg	Val	
	610					615					620					
Ile	Glu	Leu	Tyr	Ser	Arg	Ala	Glu	Lys	Lys	Leu	Ser	Gly	Ser	Val	Phe	
625					630					635					640	
Asp	Ile	Glu	Thr	Met	Phe	Arg	Glu	Tyr	Asn	Tyr	Tyr	Thr	Gln	Arg	Leu	
			645						650					655		
Ala	Gly	Leu	Arg	Glu	Asp	Leu	Asp	Asn	Thr	Ile	Asp	Leu	Asn	Arg	Asp	
		660						665					670			
Arg	Leu	Ala	Arg	Asp	Leu	Ser	Glu	Ile	Val	Ala	Asp	Leu	Gly	Asp	Val	
		675					680					685				
Gly	Arg	Thr	Val	Val	Asn	Val	Ala	Ser	Ser	Val	Ile	Thr	Leu	Phe	Gly	
	690					695					700					

Ser Ile Val Ser Gly Phe Ile Asn Phe Ile Lys Ser Pro Phe Gly Gly
705 710 715 720

Met Leu Met Ile Leu Val Ile Val Ala Val Val Leu Ile Val Phe Ala
725 730 735

Leu Asn Arg Arg Thr Asn Ala Ile Ala Gln Ala Pro Ile Arg Met Ile
740 745 750

Tyr Pro Asp Ile Asp Lys Met Gln Pro Ser Gly Gly Lys Val Asp Gln
755 760 765

Glu Gln Ile Lys Asn Ile Leu Ala Gly Met His Gln Leu Gln Gln Glu
770 775 780

Glu Arg Arg Arg Leu Asp Glu Gln Gln Arg Ser Ala Pro Ser Leu Phe
785 790 795 800

Arg Arg Ala Ser Asp Gly Leu Lys
805

<210> 39
<211> 831
<212> PRT
<213> Murine herpesvirus 68

<400> 39
Met Tyr Pro Thr Val Lys Ser Met Arg Val Ala His Leu Thr Asn Leu
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Leu Thr Leu Leu Cys Leu Leu Cys His Thr His Leu Tyr Val Cys Gln
20 25 30

Pro Thr Thr Leu Arg Gln Pro Ser Asp Met Thr Pro Ala Gln Asp Ala
35 40 45

Pro Thr Glu Thr Pro Pro Pro Leu Ser Thr Asn Thr Asn Arg Gly Phe
50 55 60

Glu Tyr Phe Arg Val Cys Gly Val Ala Ala Thr Gly Glu Thr Phe Arg
65 70 75 80

Phe Asp Leu Asp Lys Thr Cys Pro Ser Thr Gln Asp Lys Lys His Val
85 90 95

Glu Gly Ile Leu Leu Val Tyr Lys Ile Asn Ile Val Pro Tyr Ile Phe
100 105 110

Lys Ile Arg Arg Tyr Arg Lys Ile Ile Thr Gln Leu Thr Ile Trp Arg
115 120 125

Gly Leu Thr Thr Ser Ser Val Thr Gly Lys Phe Glu Met Ala Thr Gln
130 135 140

Ala His Glu Trp Glu Val Gly Asp Phe Asp Ser Ile Tyr Gln Cys Tyr
145 150 155 160

Lys	Leu	Thr	Thr	Ser	Val	Asn	Asn	Val	Leu	Glu	Glu	Leu	Ser	Arg	Ala	465	470	475	480
Trp	Cys	Arg	Glu	Gln	Val	Arg	Asp	Thr	Leu	Met	Trp	Tyr	Glu	Leu	Ser	485	490		495
Lys	Val	Asn	Pro	Thr	Ser	Val	Met	Ser	Ala	Ile	Tyr	Gly	Lys	Pro	Val	500	505		510
Ala	Ala	Arg	Tyr	Val	Gly	Asp	Ala	Ile	Ser	Val	Thr	Asp	Cys	Ile	Tyr	515	520		525
Val	Asp	Gln	Ser	Ser	Val	Asn	Ile	His	Gln	Ser	Leu	Arg	Leu	Gln	His	530	535		540
Asp	Lys	Thr	Thr	Cys	Tyr	Ser	Arg	Pro	Arg	Val	Thr	Phe	Lys	Phe	Ile	545	550	555	560
Asn	Ser	Thr	Asp	Pro	Leu	Thr	Gly	Gln	Leu	Gly	Pro	Arg	Lys	Glu	Ile	565	570		575
Ile	Leu	Ser	Asn	Thr	Asn	Ile	Glu	Thr	Cys	Lys	Asp	Glu	Ser	Glu	His	580	585		590
Tyr	Phe	Ile	Val	Gly	Glu	Tyr	Ile	Tyr	Tyr	Tyr	Lys	Asn	Tyr	Ile	Phe	595	600		605
Glu	Glu	Lys	Leu	Asn	Leu	Ser	Ser	Ile	Ala	Thr	Leu	Asp	Thr	Phe	Ile	610	615		620
Ala	Leu	Asn	Ile	Ser	Phe	Ile	Glu	Asn	Ile	Asp	Phe	Lys	Thr	Val	Glu	625	630	635	640
Leu	Tyr	Ser	Ser	Thr	Glu	Arg	Lys	Leu	Ala	Ser	Ser	Val	Phe	Asp	Ile	645	650		655
Glu	Ser	Met	Phe	Arg	Glu	Tyr	Asn	Tyr	Tyr	Thr	Tyr	Ser	Leu	Ala	Gly	660	665		670
Ile	Lys	Lys	Asp	Leu	Asp	Asn	Thr	Ile	Asp	Tyr	Asn	Arg	Asp	Arg	Leu	675	680		685
Val	Gln	Asp	Leu	Ser	Asp	Met	Met	Ala	Asp	Leu	Gly	Asp	Ile	Gly	Arg	690	695	700	
Ser	Val	Val	Asn	Val	Val	Ser	Ser	Val	Val	Thr	Phe	Phe	Ser	Ser	Ile	705	710	715	720
Val	Thr	Gly	Phe	Ile	Lys	Phe	Phe	Thr	Asn	Pro	Leu	Gly	Gly	Ile	Phe	725	730		735
Ile	Leu	Leu	Ile	Ile	Gly	Gly	Ile	Ile	Phe	Leu	Val	Val	Val	Leu	Asn	740	745		750
Arg	Arg	Asn	Ser	Gln	Phe	His	Asp	Ala	Pro	Ile	Lys	Met	Leu	Tyr	Pro	755	760	765	

Ser Val Glu Asn Tyr Ala Ala Arg Gln Ala Pro Pro Pro Tyr Ser Ala
770 775 780

Ser Pro Pro Ala Ile Asp Lys Glu Glu Ile Lys Arg Ile Leu Leu Gly
785 790 795 800

Met His Gln Val His Gln Glu Glu Lys Glu Ala Gln Lys Gln Leu Thr
805 810 815

Asn Ser Gly Pro Thr Leu Trp Gln Lys Ala Thr Gly Phe Leu Arg
820 825 830

<210> 40

<211> 844

<212> PRT

<213> Bovine herpesvirus 4

<400> 40

Tyr Tyr Lys Thr Ile Leu Phe Phe Ala Leu Ile Lys Val Cys Ser Phe
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Asn Gln Thr Thr Thr His Ser Thr Thr Thr Ser Pro Ser Ile Ser Ser
20 25 30

Thr Thr Ser Ser Thr Thr Thr Ser Thr Ser Lys Pro Ser Asn Thr Thr
35 40 45

Ser Thr Asn Ser Ser Leu Ala Ala Ser Pro Gln Asn Thr Ser Thr Ser
50 55 60

Lys Pro Ser Thr Asp Asn Gln Gly Thr Ser Thr Pro Thr Ile Pro Thr
65 70 75 80

Val Thr Asp Asp Thr Ala Ser Lys Asn Phe Tyr Lys Tyr Arg Val Cys
85 90 95

Ser Ala Ser Ser Ser Ser Gly Glu Leu Phe Arg Phe Asp Leu Asp Gln
100 105 110

Thr Cys Pro Asp Thr Lys Asp Lys Lys His Val Glu Gly Ile Leu Leu
115 120 125

Val Leu Lys Lys Asn Ile Val Pro Tyr Ile Phe Lys Val Arg Lys Tyr
130 135 140

Arg Lys Ile Ala Thr Ser Val Thr Val Tyr Arg Gly Trp Ser Gln Ala
145 150 155 160

Ala Val Thr Asn Arg Asp Asp Ile Ser Arg Ala Ile Pro Tyr Asn Glu
165 170 175

Ile Ser Met Ile Asp Arg Thr Tyr His Cys Phe Ser Ala Met Ala Thr
180 185 190

Val Ile Asn Gly Ile Leu Asn Thr Tyr Ile Asp Arg Asp Ser Glu Asn
195 200 205

Lys	Ser	Val	Pro	Leu	Gln	Pro	Val	Ala	Gly	Leu	Thr	Glu	Asn	Ile	Asn		
210						215					220						
Arg	Tyr	Phe	Ser	Gln	Pro	Leu	Ile	Tyr	Ala	Glu	Pro	Gly	Trp	Phe	Pro		
225					230					235					240		
Gly	Ile	Tyr	Arg	Val	Arg	Thr	Thr	Val	Asn	Cys	Glu	Val	Val	Asp	Met		
				245					250					255			
Tyr	Ala	Arg	Ser	Val	Glu	Pro	Tyr	Thr	His	Phe	Ile	Thr	Ala	Leu	Gly		
			260					265					270				
Asp	Thr	Ile	Glu	Ile	Ser	Pro	Phe	Cys	His	Asn	Asn	Ser	Gln	Cys	Thr		
		275					280					285					
Thr	Gly	Asn	Ser	Thr	Ser	Arg	Asp	Ala	Thr	Lys	Val	Trp	Ile	Glu	Glu		
	290					295					300						
Asn	His	Gln	Thr	Val	Asp	Tyr	Glu	Arg	Arg	Gly	His	Pro	Thr	Lys	Asp		
305					310					315					320		
Lys	Arg	Ile	Phe	Leu	Lys	Asp	Glu	Glu	Tyr	Thr	Ile	Ser	Trp	Lys	Ala		
				325					330					335			
Glu	Asp	Arg	Glu	Arg	Ala	Ile	Cys	Asp	Phe	Val	Ile	Trp	Lys	Thr	Phe		
			340					345					350				
Pro	Arg	Ala	Ile	Gln	Thr	Ile	His	Asn	Glu	Ser	Phe	His	Phe	Val	Ala		
		355					360					365					
Asn	Glu	Val	Thr	Ala	Ser	Phe	Leu	Thr	Ser	Asn	Gln	Glu	Glu	Thr	Glu		
	370					375					380						
Leu	Arg	Gly	Asn	Thr	Glu	Ile	Leu	Asn	Cys	Met	Asn	Ser	Thr	Ile	Asn		
385					390					395					400		
Glu	Thr	Leu	Glu	Glu	Thr	Val	Lys	Lys	Phe	Asn	Lys	Ser	His	Ile	Arg		
				405					410					415			
Asp	Gly	Glu	Val	Lys	Tyr	Tyr	Lys	Thr	Asn	Gly	Gly	Leu	Phe	Leu	Ile		
			420					425					430				
Trp	Gln	Ala	Met	Lys	Pro	Leu	Asn	Leu	Ser	Glu	His	Thr	Asn	Tyr	Thr		
		435					440					445					
Ile	Glu	Arg	Asn	Asn	Lys	Thr	Gly	Asn	Lys	Ser	Arg	Gln	Lys	Arg	Ser		
	450					455					460						
Val	Asp	Thr	Lys	Thr	Phe	Gln	Gly	Ala	Lys	Gly	Leu	Ser	Thr	Ala	Gln		
465					470					475					480		
Val	Gln	Tyr	Ala	Tyr	Asp	His	Leu	Arg	Thr	Ser	Met	Asn	His	Ile	Leu		
				485					490					495			
Glu	Glu	Leu	Thr	Lys	Thr	Trp	Cys	Arg	Glu	Gln	Lys	Lys	Asp	Asn	Leu		
			500					505					510				

Met	Trp	Tyr	Glu	Leu	Ser	Lys	Ile	Asn	Pro	Val	Ser	Val	Met	Ala	Ala		
		515					520					525					
Ile	Tyr	Gly	Lys	Pro	Val	Ala	Val	Lys	Ala	Met	Gly	Asp	Ala	Phe	Met		
	530					535					540						
Val	Ser	Glu	Cys	Ile	Asn	Val	Asp	Gln	Ala	Ser	Val	Asn	Ile	His	Lys		
545					550					555					560		
Ser	Met	Arg	Thr	Asp	Asp	Pro	Lys	Val	Cys	Tyr	Ser	Arg	Pro	Leu	Val		
				565					570					575			
Thr	Phe	Lys	Phe	Val	Asn	Ser	Thr	Ala	Thr	Phe	Arg	Gly	Gln	Leu	Gly		
			580					585					590				
Thr	Arg	Asn	Glu	Ile	Leu	Leu	Thr	Asn	Thr	His	Val	Glu	Thr	Cys	Arg		
		595					600					605					
Pro	Thr	Ala	Asp	His	Tyr	Phe	Phe	Val	Lys	Asn	Met	Thr	His	Tyr	Phe		
	610					615					620						
Lys	Asp	Tyr	Lys	Phe	Val	Lys	Thr	Met	Asp	Thr	Asn	Asn	Ile	Ser	Thr		
625					630					635					640		
Leu	Asp	Thr	Phe	Leu	Thr	Leu	Asn	Leu	Thr	Phe	Ile	Asp	Asn	Ile	Asp		
				645					650					655			
Phe	Lys	Thr	Val	Glu	Leu	Tyr	Ser	Glu	Thr	Glu	Arg	Lys	Met	Ala	Ser		
			660					665					670				
Ala	Leu	Asp	Leu	Glu	Thr	Met	Phe	Arg	Glu	Tyr	Asn	Tyr	Tyr	Thr	Gln		
		675					680					685					
Lys	Leu	Ala	Ser	Leu	Arg	Glu	Asp	Leu	Asp	Asn	Thr	Ile	Asp	Leu	Asn		
	690					695					700						
Arg	Asp	Arg	Leu	Val	Lys	Asp	Leu	Ser	Glu	Met	Met	Ala	Asp	Leu	Gly		
705					710					715					720		
Asp	Ile	Gly	Lys	Val	Val	Val	Asn	Thr	Phe	Ser	Gly	Ile	Val	Thr	Val		
			725						730					735			
Phe	Gly	Ser	Ile	Val	Gly	Gly	Phe	Val	Ser	Phe	Phe	Thr	Asn	Pro	Ile		
			740					745					750				
Gly	Gly	Val	Thr	Ile	Ile	Leu	Leu	Leu	Ile	Val	Val	Val	Phe	Val	Val		
		755					760					765					
Phe	Ile	Val	Ser	Arg	Arg	Thr	Asn	Asn	Met	Asn	Glu	Ala	Pro	Ile	Lys		
	770					775					780						
Met	Ile	Tyr	Pro	Asn	Ile	Asp	Lys	Ala	Ser	Glu	Gln	Glu	Asn	Ile	Gln		
785					790					795					800		
Pro	Leu	Pro	Gly	Glu	Glu	Ile	Lys	Arg	Ile	Leu	Leu	Gly	Met	His	Gln		
				805					810					815			

Ser	Asp	Val	Leu	Ser	Ser	Gln	Val	Asp	Phe	Asn	His	Thr	Val	Val	Asp	245	250	255	
Tyr	Gly	Asn	Arg	Ala	Thr	Ser	Gln	Gln	His	Gly	Lys	Arg	Ile	Phe	Ala	260	265	270	
His	Thr	Leu	Asp	Tyr	Ser	Val	Ser	Trp	Glu	Ala	Ile	Asn	Lys	Thr	Thr	275	280	285	
Ser	Val	Cys	Ser	Met	Val	Phe	Trp	Lys	Gly	Phe	Gln	Arg	Ala	Ile	Gln	290	295	300	
Thr	Glu	His	Asp	Ser	Thr	Tyr	His	Phe	Ile	Ala	Asn	Glu	Ile	Thr	Ala	305	310	315	320
Gly	Phe	Ser	Thr	Ser	Lys	Glu	Thr	Leu	Ala	Ser	Phe	Ser	Ser	Glu	Tyr	325	330	335	
Ser	Cys	Leu	Met	Ser	Asp	Ile	Asn	Ser	Thr	Leu	Thr	Asp	Lys	Ile	Gly	340	345	350	
Arg	Val	Asn	Asn	Thr	His	Val	Pro	Asn	Gly	Thr	Ala	Gln	Tyr	Phe	Lys	355	360	365	
Thr	Glu	Gly	Gly	Met	Ile	Leu	Val	Trp	Gln	Pro	Leu	Thr	Ala	Ile	Glu	370	375	380	
Leu	Glu	Glu	Ala	Met	Ile	Glu	Ala	Thr	Thr	Val	Ser	Pro	Thr	Pro	Leu	385	390	395	400
Ser	Thr	Ala	His	Leu	Thr	Ser	Arg	Arg	Thr	Gly	Arg	Arg	Lys	Arg	Asp	405	410	415	
Val	Ser	Ala	Gly	Ser	Glu	Asn	Ser	Val	Leu	Leu	Ala	Gln	Ile	Gln	Tyr	420	425	430	
Ala	Tyr	Asp	Lys	Leu	Arg	Gln	Ser	Ile	Asn	Asn	Val	Leu	Glu	Glu	Leu	435	440	445	
Ala	Ile	Thr	Trp	Cys	Arg	Glu	Gln	Val	Arg	Gln	Thr	Met	Ile	Trp	Tyr	450	455	460	
Glu	Ile	Ala	Lys	Ile	Asn	Pro	Thr	Ser	Val	Met	Thr	Ala	Ile	Tyr	Gly	465	470	475	480
Lys	Pro	Val	Ser	Ala	Lys	Ala	Leu	Gly	Asp	Val	Ile	Ser	Val	Thr	Glu	485	490	495	
Cys	Ile	Asn	Val	Asp	Gln	Thr	Ser	Val	Ser	Ile	His	Lys	Ser	Leu	Lys	500	505	510	
Thr	Thr	Asn	Asn	Asp	Val	Cys	Tyr	Ser	Arg	Pro	Pro	Val	Thr	Phe	Lys	515	520	525	
Phe	Val	Asn	Ser	Ser	Gln	Leu	Phe	Lys	Gly	Gln	Leu	Gly	Ala	Arg	Asn	530	535	540	

Glu Ile Leu Leu Ser Glu Ser Leu Val Glu Asn Cys His Gln Asn Ala
 545 550 555 560
 Glu His Phe Phe Thr Ala Lys Asn Glu Thr Tyr His Phe Lys Asn Tyr
 565 570 575
 Leu His Val Glu Thr Leu Pro Leu Thr Asn Ile Ser Thr Leu Asp Thr
 580 585 590
 Phe Leu Ala Leu Asn Leu Thr Phe Ile Glu Asn Ile Asp Phe Lys Ala
 595 600 605
 Val Glu Leu Tyr Ser Ser Gly Glu Arg Lys Leu Ala Asn Val Phe Asp
 610 615 620
 Leu Glu Thr Met Phe Arg Glu Tyr Asn Tyr Tyr Ala Gln Ser Ile Ser
 625 630 635 640
 Gly Leu Arg Lys Asp Phe Asp Asn Ser Gln Arg Asn Asn Arg Asp Arg
 645 650 655
 Ile Ile Gln Asp Phe Ser Glu Ile Leu Ala Asp Leu Gly Ser Ile Gly
 660 665 670
 Lys Val Ile Val Asn Ile Ala Ser Ser Ala Phe Ser Leu Phe Gly Gly
 675 680 685
 Ile Val Thr Gly Ile Leu Asn Phe Ile Lys Asn Pro Leu Gly Gly Met
 690 695 700
 Leu Thr Phe Leu Leu Val Gly Ala Ile Ile Ile Leu Val Ile Leu Leu
 705 710 715 720
 Val Arg Arg Thr Asn Asn Met Ser Gln Ala Pro Ile Arg Met Ile Tyr
 725 730 735
 Pro Asp Ile Glu Lys Ser Arg Ser Ser Val Thr Pro Thr Glu Pro Glu
 740 745 750
 Val Ile Lys Gln Ile Leu Leu Gly Met His Asn Met Gln Gln Glu Glu
 755 760 765
 Tyr Lys Lys Arg Glu Glu His Lys Ala Ser Gln Pro Ser Phe Leu Lys
 770 775 780
 Arg Ala Thr Asp Ala Phe Leu
 785 790
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 Met Val Pro Asn Lys His Leu Leu Leu Ile Ile Leu Ser Phe Ser Thr
 1 5 10 15

Gly	Phe	Ser	Thr	Val	Lys	Glu	Pro	Leu	Ala	Asn	Phe	Thr	Ser	Asp	Tyr	325	330	335	
Asn	Cys	Leu	Met	Thr	His	Ile	Asn	Thr	Thr	Leu	Glu	Asp	Lys	Ile	Ala	340	345	350	
Arg	Val	Asn	Asn	Thr	His	Thr	Pro	Asn	Gly	Thr	Ala	Glu	Tyr	Tyr	Gln	355	360	365	
Thr	Glu	Gly	Gly	Met	Ile	Leu	Val	Trp	Gln	Pro	Leu	Ile	Ala	Ile	Glu	370	375	380	
Leu	Glu	Glu	Ala	Met	Leu	Glu	Ala	Thr	Thr	Ser	Pro	Val	Thr	Pro	Ser	385	390	395	400
Ala	Pro	Thr	Ser	Ser	Ser	Arg	Ser	Lys	Arg	Ala	Ile	Arg	Ser	Ile	Arg	405	410	415	
Asp	Val	Ser	Ala	Gly	Ser	Glu	Asn	Asn	Val	Phe	Leu	Ser	Gln	Ile	Gln	420	425	430	
Tyr	Ala	Tyr	Asp	Lys	Leu	Arg	Gln	Ser	Ile	Asn	Asn	Val	Leu	Glu	Glu	435	440	445	
Leu	Ala	Ile	Thr	Trp	Cys	Arg	Glu	Gln	Val	Arg	Gln	Thr	Met	Val	Trp	450	455	460	
Tyr	Glu	Ile	Ala	Lys	Ile	Asn	Pro	Thr	Ser	Val	Met	Thr	Ala	Ile	Tyr	465	470	475	480
Gly	Lys	Pro	Val	Ser	Arg	Lys	Ala	Leu	Gly	Asp	Val	Ile	Ser	Val	Thr	485	490	495	
Glu	Cys	Ile	Asn	Val	Asp	Gln	Ser	Ser	Val	Ser	Ile	His	Lys	Ser	Leu	500	505	510	
Lys	Thr	Glu	Asn	Asn	Asp	Ile	Cys	Tyr	Ser	Arg	Pro	Pro	Val	Thr	Phe	515	520	525	
Lys	Phe	Val	Asn	Ser	Ser	Gln	Leu	Phe	Lys	Gly	Gln	Leu	Gly	Ala	Arg	530	535	540	
Asn	Glu	Ile	Leu	Leu	Ser	Glu	Ser	Leu	Val	Glu	Asn	Cys	His	Gln	Asn	545	550	555	560
Ala	Glu	Thr	Phe	Phe	Thr	Ala	Lys	Asn	Glu	Thr	Tyr	His	Phe	Lys	Asn	565	570	575	
Tyr	Val	His	Val	Glu	Thr	Leu	Pro	Val	Asn	Asn	Ile	Ser	Thr	Leu	Asp	580	585	590	
Thr	Phe	Leu	Ala	Leu	Asn	Leu	Thr	Phe	Ile	Glu	Asn	Ile	Asp	Phe	Lys	595	600	605	
Ala	Val	Glu	Leu	Tyr	Ser	Ser	Gly	Glu	Arg	Lys	Leu	Ala	Asn	Val	Phe	610	615	620	

Asp Leu Glu Thr Met Phe Arg Glu Tyr Asn Tyr Tyr Ala Gln Ser Ile
625 630 635 640

Ser Gly Leu Arg Lys Asp Phe Asp Asn Ser Gln Arg Asn Asn Arg Asp
645 650 655

Arg Ile Ile Gln Asp Phe Ser Glu Ile Leu Ala Asp Leu Gly Ser Ile
660 665 670

Gly Lys Val Ile Val Asn Val Ala Ser Gly Ala Phe Ser Leu Phe Gly
675 680 685

Gly Ile Val Thr Gly Ile Leu Asn Phe Ile Lys Asn Pro Leu Gly Gly
690 695 700

Met Phe Thr Phe Leu Leu Ile Gly Ala Val Ile Ile Leu Val Ile Leu
705 710 715 720

Leu Val Arg Arg Thr Asn Asn Met Ser Gln Ala Pro Ile Arg Met Ile
725 730 735

Tyr Pro Asp Val Glu Lys Ser Lys Ser Thr Val Thr Pro Met Glu Pro
740 745 750

Glu Thr Ile Lys Gln Ile Leu Leu Gly Met His Asn Met Gln Gln Glu
755 760 765

Ala Tyr Lys Lys Lys Glu Glu Gln Arg Ala Ala Arg Pro Ser Ile Phe
770 775 780

Arg Gln Ala Ala Glu Thr Phe Leu
785 790

<210> 43
<211> 824
<212> PRT
<213> Equine herpesvirus 2

<400> 43
Met Gly Val Gly Gly Gly Pro Arg Val Val Leu Cys Leu Trp Cys Val
1 5 10 15

Ala Ala Leu Leu Cys Gln Gly Val Ala Gln Glu Val Val Ala Glu Thr
20 25 30

Thr Thr Pro Phe Ala Thr His Arg Pro Glu Val Val Ala Glu Glu Asn
35 40 45

Pro Ala Asn Pro Phe Leu Pro Phe Arg Val Cys Gly Ala Ser Pro Thr
50 55 60

Gly Gly Glu Ile Phe Arg Phe Pro Leu Glu Glu Ser Cys Pro Asn Thr
65 70 75 80

Glu Asp Lys Asp His Ile Glu Gly Ile Ala Leu Ile Tyr Lys Thr Asn
85 90 95

Thr	Ser	Gln	Val	Gln	Phe	Ala	Tyr	Asp	Gln	Leu	Arg	Lys	Ser	Ile	Asn	
450						455					460					
Arg	Val	Leu	Glu	Gln	Leu	Ser	Arg	Val	Trp	Cys	Gln	Asn	Gln	Tyr	Arg	
465					470					475					480	
Ala	Ser	Leu	Met	Trp	Tyr	Glu	Leu	Ser	Lys	Ile	Asn	Pro	Thr	Ser	Val	
				485					490					495		
Met	Ser	Ala	Ile	Tyr	Gly	Arg	Pro	Val	Ser	Ala	Lys	Leu	Val	Gly	Asp	
			500					505					510			
Val	Val	Gln	Ile	Ser	Asp	Cys	Ile	Thr	Val	Asp	Gln	Glu	Ser	Val	Phe	
		515					520					525				
Val	His	Arg	Asn	Leu	Arg	Val	Pro	Gly	Ser	Lys	Asp	Leu	Cys	Tyr	Thr	
	530					535					540					
Arg	Pro	Val	Val	Gly	Phe	Lys	Phe	Ile	Asn	Gly	Ser	Glu	Leu	Phe	Val	
545					550					555					560	
Gly	Gln	Leu	Gly	Ala	Arg	Asn	Glu	Ile	Leu	Leu	Ser	Thr	Asn	Leu	Val	
				565					570					575		
Glu	Val	Cys	Gln	His	Ser	Cys	Glu	His	Tyr	Phe	Gln	Gly	Gly	Asn	His	
			580					585					590			
Ile	Tyr	Lys	Tyr	Lys	Asn	Tyr	Glu	Tyr	Val	Ser	Thr	Met	Asn	Leu	Thr	
		595					600					605				
Asp	Val	Pro	Thr	Leu	His	Thr	Met	Ile	Thr	Leu	Asn	Leu	Ser	Leu	Val	
	610					615					620					
Glu	Asn	Val	Asp	Phe	Gln	Val	Ile	Gln	Leu	Tyr	Ser	Gln	Lys	Glu	Lys	
625					630					635					640	
Lys	Leu	Ser	Asn	Val	Phe	Asp	Ile	Glu	Thr	Met	Phe	Arg	Glu	Tyr	Asn	
				645					650					655		
Tyr	Tyr	Thr	Gln	Asn	Leu	Lys	Gly	Leu	Arg	Lys	Asp	Leu	Asp	Asp	Ser	
			660					665					670			
Ile	His	Asp	Gly	Arg	Asp	Ser	Phe	Ile	Gln	Phe	Leu	Gly	Asp	Leu	Val	
		675					680					685				
Gln	Asp	Leu	Val	Pro	Val	Gly	Asp	Val	Ile	Val	Asn	Val	Ala	Ser	Gly	
	690					695					700					
Val	Phe	Ser	Leu	Phe	Gly	Ser	Ile	Val	Ser	Gly	Val	Ile	Ser	Phe	Leu	
705					710					715					720	
Lys	Asn	Pro	Leu	Gly	Ala	Ile	Leu	Thr	Ile	Ala	Leu	Ile	Val	Gly	Gly	
				725					730					735		
Ile	Ile	Val	Leu	Tyr	Leu	Phe	Ile	Thr	Arg	Ser	Arg	Thr	Val	Tyr	Gln	
			740					745					750			

Asn	Ser	Val	Arg	Arg	Tyr	His	Ser	Gln	Pro	Glu	Ile	His	Ala	Glu	Pro	195	200	205	
Gly	Trp	Leu	Leu	Gly	Gly	Tyr	Arg	Arg	Arg	Thr	Thr	Val	Asn	Cys	Glu	210	215	220	
Val	Thr	Glu	Thr	Asp	Ala	Arg	Ala	Val	Pro	Pro	Phe	Arg	Tyr	Phe	Ile	225	230	235	240
Thr	Asn	Ile	Gly	Asp	Thr	Ile	Glu	Met	Ser	Pro	Phe	Trp	Ser	Lys	Ala	245	250	255	
Trp	Asn	Glu	Thr	Glu	Phe	Ser	Gly	Glu	Pro	Asp	Arg	Thr	Leu	Thr	Val	260	265	270	
Ala	Lys	Asp	Tyr	Arg	Val	Val	Asp	Tyr	Lys	Phe	Arg	Gly	Thr	Gln	Pro	275	280	285	
Gln	Gly	His	Thr	Arg	Ile	Phe	Val	Asp	Lys	Glu	Glu	Tyr	Thr	Leu	Ser	290	295	300	
Trp	Ala	Gln	Gln	Phe	Arg	Asn	Ile	Ser	Tyr	Cys	Arg	Trp	Ala	His	Trp	305	310	315	320
Lys	Ser	Phe	Asp	Asn	Ala	Ile	Lys	Thr	Glu	His	Gly	Lys	Ser	Leu	His	325	330	335	
Phe	Val	Ala	Asn	Asp	Ile	Thr	Ala	Ser	Phe	Tyr	Thr	Pro	Asn	Thr	Gln	340	345	350	
Thr	Arg	Glu	Val	Leu	Gly	Lys	His	Val	Cys	Leu	Asn	Asn	Thr	Ile	Glu	355	360	365	
Ser	Glu	Leu	Lys	Ser	Arg	Leu	Ala	Lys	Val	Asn	Asp	Thr	His	Ser	Pro	370	375	380	
Asn	Gly	Thr	Ala	Gln	Tyr	Tyr	Leu	Thr	Asn	Gly	Gly	Leu	Leu	Leu	Val	385	390	395	400
Trp	Gln	Pro	Leu	Val	Gln	Gln	Lys	Leu	Leu	Asp	Ala	Lys	Gly	Leu	Leu	405	410	415	
Asp	Ala	Val	Lys	Lys	Gln	Gln	Asn	Thr	Thr	Thr	Thr	Thr	Thr	Thr	Thr	420	425	430	
Arg	Ser	Arg	Arg	Gln	Arg	Arg	Ser	Val	Ser	Ser	Gly	Ile	Asp	Asp	Val	435	440	445	
Tyr	Thr	Ala	Glu	Ser	Thr	Ile	Leu	Leu	Thr	Gln	Ile	Gln	Phe	Ala	Tyr	450	455	460	
Asp	Thr	Leu	Arg	Ala	Gln	Ile	Asn	Asn	Val	Leu	Glu	Glu	Leu	Ser	Arg	465	470	475	480
Ala	Trp	Cys	Arg	Glu	Gln	His	Arg	Ala	Ser	Leu	Met	Trp	Asn	Glu	Leu	485	490	495	

<213> artificial

<220>

<223> Suid herpesvirus 1 - bases 641-1300

<400> 47

cgccgcccgtc	eggctccacg	gtgggtgcggc	tggagcccga	gcaggcctgc	cccaggtact	60
cgcagggggcg	caacttcacg	gaggggatcg	ccgtgctctt	caaggagaac	atcgccccgc	120
acaagttcaa	ggcccacatc	tactacaaga	acgtcatcgt	cacgaccgtg	tggtccggga	180
gcacgtacgc	ggccatcacg	aaccgcttca	cagaccgcgt	gcccgtcccc	gtgcaggaga	240
tcacggacgt	gatcgaccgc	cgcggcaagt	gcgtctccaa	ggccgagtac	gtgcgcaaca	300
accacaaggt	gaccgccttc	gaccgcgacg	agaacccccg	cgaggtggac	ctgcgcccct	360
cgcgcctgaa	cgcgctcggc	acccgcggct	ggcacaccac	caacgacacc	tacaccaaga	420
tggcgccgcg	gggcttctac	cacacgggca	cctccgtcaa	ctgcatcgtc	gaggaggtgg	480
aggcgcgctc	cgtgtacccc	tacgactcct	tcgccctgtc	cacgggggac	attgtgtaca	540
tgtccccctt	ctacggcctg	cgcgaggggg	cccacgggga	gcacatcggc	tacgcgcccg	600
ggcgcttcca	gcaggtggag	cactactacc	ccatcgacct	ggactcgcgc	ctccgcgcct	660

<210> 48

<211> 359

<212> PRT

<213> artificial

<220>

<223> Suid herpesvirus 1 - bases 491-850

<400> 48

Ala	Ala	Pro	Ala	Ala	Ala	Arg	Arg	Ala	Arg	Arg	Ser	Pro	Gly	Pro	Ala	
1				5					10					15		
Gly	Thr	Pro	Glu	Pro	Pro	Ala	Val	Asn	Gly	Thr	Gly	His	Leu	Arg	Ile	
			20					25					30			
Thr	Thr	Gly	Ser	Ala	Glu	Phe	Ala	Arg	Leu	Gln	Phe	Thr	Tyr	Asp	His	
		35					40					45				
Ile	Gln	Ala	His	Val	Asn	Asp	Met	Leu	Gly	Arg	Ile	Ala	Ala	Ala	Trp	
	50					55					60					
Cys	Glu	Leu	Gln	Asn	Lys	Asp	Arg	Thr	Leu	Trp	Ser	Glu	Met	Ser	Arg	
65					70					75					80	
Leu	Asn	Pro	Ser	Ala	Val	Ala	Thr	Ala	Ala	Leu	Gly	Gln	Arg	Val	Ser	
				85					90					95		
Ala	Arg	Met	Leu	Gly	Asp	Val	Met	Ala	Ile	Ser	Arg	Cys	Val	Glu	Val	
		100						105					110			
Arg	Gly	Gly	Val	Tyr	Val	Gln	Asn	Ser	Met	Arg	Val	Pro	Gly	Glu	Arg	
		115					120					125				
Gly	Thr	Cys	Tyr	Ser	Arg	Pro	Leu	Val	Thr	Phe	Glu	His	Asn	Gly	Thr	
	130					135					140					
Gly	Val	Ile	Glu	Gly	Gln	Leu	Gly	Asp	Asp	Asn	Glu	Leu	Leu	Ile	Ser	
145					150					155					160	

<212> PRT
 <213> Suid herpesvirus 2

<400> 50
 Ser Ile Met Ile Ala Asn Asn Leu Cys Tyr Ser Thr Leu Ile Leu Asn
 1 5 10 15
 Asp Glu Asp Val Thr Gly Ile Asp Glu Lys Asp Ile Leu Thr Val His
 20 25 30
 Val Asn Lys Asn Thr Val Tyr Arg Phe Val Arg Ser Ser Val Arg Glu
 35 40 45
 Ser Ile Leu Gly Thr Leu Leu Ser Arg Trp Leu Arg Lys Arg Lys Glu
 50 55 60
 Val Lys Ala Arg Met Lys Arg Cys Glu Asp Pro Met Leu Ala Leu Ile
 65 70 75 80
 Leu Asp Lys Gln Gln Leu Ala Leu Lys Val Thr Cys Asn Ala Phe Tyr
 85 90 95
 Gly Phe Thr Gly Ala Val His Gly Leu Leu Pro Cys Leu Pro Leu Ala
 100 105 110
 Ala Ser Ile Thr Ser Ile Gly Arg Asp Met Leu Arg Gln Thr Ser Asp
 115 120 125
 Phe Ile Asn Asn Val Leu Ser Ser Arg Glu Tyr Val Ser Glu Lys Phe
 130 135 140
 Ser Leu Ser Asp Gly Asp Phe Gln Gly Asp Phe Ser Pro Glu Cys
 145 150 155

<210> 51
 <211> 466
 <212> DNA
 <213> artificial

<220>
 <223> Portion of porcine gamma herpesvirus polymerase - AF118399

<400> 51
 taatctatgt cactctaccc taatccatca tgaagacctg cataaatatc ctcaattaaa 60
 ggaggaggat tatgaaacat ttttgattag ttctggctct gttcactttg taaaaaaaca 120
 catatcagaa tctcttctgt ctaacctgct tacaacatgg ctggctaaga gaaaaatgat 180
 cagaaaggaa ttagcagcat gtgctgaccc aaagctcagg acaatttttag ataaacagca 240
 gcttgcaatt aaggtgacat gcaatgctgt gtatgggttc actggtggtg catctggtat 300
 gctgcctgt ctcaagattg cagagaccat aactatgcaa ggaagggcca tgttgaaaa 360
 gacaaaagta tttgtagaga atttaagtca tgaggatctc cattccatct gtaagggttg 420
 ctttatgcct cagtcaccaa acagcattga taaacccttc aaggtg 466

<210> 52
 <211> 423
 <212> DNA
 <213> artificial

<220>

<223> Portion of porcine gamma herpesvirus polymerase - AF118401

<400> 52

gaggacctgc	ataagtatcc	tcaattaaag	gaggatgatt	atgaaacatt	tttgattagt	60
tctggccctg	ttcactttgt	aaaaaaacac	atatacagaat	ctcttctgtc	gaacttgctc	120
acaacatggc	tggccaagag	aaaaatgac	agaaaggaat	tgacagcatg	tgctgatcca	180
aagctcagga	caattttaga	taaacagcag	cttgcaatta	aggtgacatg	caatgctgtg	240
tatggattca	ctggtgttgc	atctggtatg	ctgccatgtc	tcaagattgc	agagaccatc	300
actatgcaag	gaagggccat	gttggaag	acaaaagtat	ttgtagagaa	tctgagtcac	360
gaagatctcc	gttccatag	taagggtggc	tctatacctc	agtcacaaa	cgtgtttgat	420
aaa						423

<210> 53

<211> 292

<212> DNA

<213> artificial

<220>

<223> Portion of Acelaphine herpesvirus.

<400> 53

aagtaataga	actatactct	agagaagaga	agaggatgag	cactgcattt	gatatagaga	60
ccatgtttag	agaatacaac	tactacacac	agagggtcac	tggcctgcgg	agggacttga	120
cagacctagc	tacaaacaga	aatcaatttg	tagatgcctt	tggcagcctc	atggacgact	180
tgggggtcgt	ggggaaaacg	gtgttgaatg	ctgtgagcag	tgtggccaca	ctcttcagct	240
ctatagtctc	agggatcatc	aatttcatta	aaaaccctt	tgggggaatg	tt	292

<210> 54

<211> 152

<212> DNA

<213> artificial

<220>

<223> Portion of Acelaphine herpesvirus.

<400> 54

tgggtccgtg	agcagcaccg	agcctctctc	atgtggaacg	agctaagcaa	aatcaaccct	60
accagtgtga	tgagctctat	atcggggcgg	ccagtatctg	ccaaaagaat	tggagatgtg	120
atatctgtct	ctcactgtgt	ggtggtggac	ca			152

<210> 55

<211> 793

<212> PRT

<213> artificial

<220>

<223> Portion of Acelaphine herpesvirus.

<400> 55

Lys	Gly	Ile	His	Ser	Asp	Pro	Ser	Ala	Phe	Pro	Phe	Arg	Val	Cys	Ser
1				5					10					15	

Leu Ala Lys Val Asn Asp Thr His Ser Pro Asn Gly Thr Ala Gln Tyr
 325 330 335
 Tyr Leu Thr Asn Gly Gly Leu Leu Leu Val Trp Gln Pro Leu Val Gln
 340 345 350
 Gln Lys Leu Leu Asp Ala Lys Gly Leu Leu Asp Ala Val Lys Lys Gln
 355 360 365
 Gln Asn Thr Thr Thr Thr Thr Thr Thr Arg Ser Arg Arg Gln Arg
 370 375 380
 Arg Ser Val Ser Ser Gly Ile Asp Asp Val Tyr Thr Ala Glu Ser Thr
 385 390 395 400
 Ile Leu Leu Thr Gln Ile Gln Phe Ala Tyr Asp Thr Leu Arg Ala Gln
 405 410 415
 Ile Asn Asn Val Leu Glu Glu Leu Ser Arg Ala Trp Cys Arg Glu Gln
 420 425 430
 His Arg Ala Ser Leu Met Trp Asn Glu Leu Ser Lys Ile Asn Pro Thr
 435 440 445
 Ser Val Met Ser Ser Ile Tyr Gly Arg Pro Val Ser Ala Lys Arg Ile
 450 455 460
 Gly Asp Val Ile Ser Val Ser His Cys Val Val Val Asp Gln Asp Ser
 465 470 475 480
 Val Ser Leu His Arg Ser Met Arg Val Pro Gly Arg Asp Lys Thr His
 485 490 495
 Glu Cys Tyr Ser Arg Pro Pro Val Thr Phe Lys Phe Ile Asn Asp Ser
 500 505 510
 His Leu Tyr Lys Gly Gln Leu Gly Val Asn Asn Glu Ile Leu Leu Thr
 515 520 525
 Thr Thr Ala Val Glu Ile Cys His Glu Asn Thr Glu His Tyr Phe Gln
 530 535 540
 Gly Gly Asn Asn Met Tyr Phe Tyr Lys Asn Tyr Arg His Val Lys Thr
 545 550 555 560
 Met Pro Val Gly Asp Val Ala Thr Leu Asp Thr Phe Met Val Leu Asn
 565 570 575
 Leu Thr Leu Val Glu Asn Ile Asp Phe Gln Val Ile Glu Leu Tyr Ser
 580 585 590
 Arg Glu Glu Lys Arg Met Ser Thr Ala Phe Asp Ile Glu Thr Met Phe
 595 600 605
 Arg Glu Tyr Asn Tyr Tyr Thr Gln Arg Val Thr Gly Leu Arg Arg Asp
 610 615 620

Leu Thr Asp Leu Ala Thr Asn Arg Asn Gln Phe Val Asp Ala Phe Gly
625 630 635 640

Ser Leu Met Asp Asp Leu Gly Val Val Gly Lys Thr Val Leu Asn Ala
645 650 655

Val Ser Ser Val Ala Thr Leu Phe Ser Ser Ile Val Ser Gly Ile Ile
660 665 670

Asn Phe Ile Lys Asn Pro Phe Gly Gly Met Leu Leu Phe Gly Leu Ile
675 680 685

Ala Ala Val Val Ile Thr Val Ile Leu Leu Asn Arg Lys Ala Lys Arg
690 695 700

Phe Ala Gln Asn Pro Val Gln Met Ile Pro Asp Ile Lys Thr Ile Thr
705 710 715 720

Ser Gln Arg Glu Glu Leu Gln Val Asp Pro Ile Ser Lys His Glu Leu
725 730 735

Asp Arg Ile Met Leu Ala Met His Asp Tyr His Ala Ser Lys Gln Pro
740 745 750

Glu Ser Lys Gln Asp Glu Glu Gln Gly Ser Thr Thr Ser Gly Pro Ala
755 760 765

Asp Leu Asn Lys Ala Lys Asn Val Leu Arg Arg Arg Ala Gly Tyr Lys
770 775 780

Pro Leu Lys Arg Thr Asp Ser Phe Glu
785 790

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